

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 09/658, 699 A  
Source: IFW16  
Date Processed by STIC: 02/08/2006

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 02/13/2006

PATENT APPLICATION: US/09/658,699A

TIME: 13:51:06

Input Set : A:\16622-005001.txt

Output Set: N:\CRF4\02132006\I658699A.raw

```

4 <110> APPLICANT: Oppmann, Birgit
5     De Waal Malefyt, Rene
6     Rennick, Donna M.
7     Kastelein, Robert A.
8     Wiekowski, Maria T.
9     Lira, Sergio A.
10    Narula, Satwant K.
13 <120> TITLE OF INVENTION: Mammalian Genes; Related Reagents and
14    Methods
16 <130> FILE REFERENCE: 16622-005001/DX01042X
18 <140> CURRENT APPLICATION NUMBER: US 09/658,699A
19 <141> CURRENT FILING DATE: 2000-09-08
21 <150> PRIOR APPLICATION NUMBER: US 60/164,616
22 <151> PRIOR FILING DATE: 1999-11-10
24 <150> PRIOR APPLICATION NUMBER: US 60/153,281
25 <151> PRIOR FILING DATE: 1999-09-09
27 <160> NUMBER OF SEQ ID NOS: 36
29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 570
33 <212> TYPE: DNA
34 <213> ORGANISM: Unknown Organism
36 <220> FEATURE:
37 <223> OTHER INFORMATION: Description of Unknown Organism: surmised Homo
38    sapiens
40 <220> FEATURE:
41 <221> NAME/KEY: CDS
42 <222> LOCATION: (1)..(567)
44 <220> FEATURE:
45 <221> NAME/KEY: mat_peptide
46 <222> LOCATION: (64)..(567)
48 <400> SEQUENCE: 1
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50 Met Leu Gly Ser Arg Ala Val Met Leu Leu Leu Leu Leu Pro Trp Thr
51   -20                               -15                               -10
53 gct cag ggc aga gct gtg cct ggg ggc agc agc cct gcc tgg act cag      96
54 Ala Gln Gly Arg Ala Val Pro Gly Gly Ser Ser Pro Ala Trp Thr Gln
55   -5                               -1    1                               5                               10
57 tgc cag cag ctt tca cag aag ctg tgc aca ctg gcc tgg agt gca cat      144
58 Cys Gln Gln Leu Ser Gln Lys Leu Cys Thr Leu Ala Trp Ser Ala His
59   15                               20                               25
61 cca cta gtg gga cac atg gat cta aga gaa gag gga gat gaa gag act      192
62 Pro Leu Val Gly His Met Asp Leu Arg Glu Glu Gly Asp Glu Glu Thr

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63          30          35          40
65 aca aat gat gtt ccc cat atc cag tgt gga gat ggc tgt gac ccc caa 240
66 Thr Asn Asp Val Pro His Ile Gln Cys Gly Asp Gly Cys Asp Pro Gln
67          45          50          55
69 gga ctc agg gac aac agt cag ttc tgc ttg caa agg atc cac cag ggt 288
70 Gly Leu Arg Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile His Gln Gly
71 60          65          70          75
73 ctg att ttt tat gag aag ctg cta gga tcg gat att ttc aca ggg gag 336
74 Leu Ile Phe Tyr Glu Lys Leu Leu Gly Ser Asp Ile Phe Thr Gly Glu
75          80          85          90
77 cct tct ctg ctc cct gat agc cct gtg gcg cag ctt cat gcc tcc cta 384
78 Pro Ser Leu Leu Pro Asp Ser Pro Val Ala Gln Leu His Ala Ser Leu
79          95          100          105
81 ctg ggc ctc agc caa ctc ctg cag cct gag ggt cac cac tgg gag act 432
82 Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Gly His His Trp Glu Thr
83          110          115          120
85 cag cag att cca agc ctc agt ccc agc cag cca tgg cag cgt ctc ctt 480
86 Gln Gln Ile Pro Ser Leu Ser Pro Ser Gln Pro Trp Gln Arg Leu Leu
87          125          130          135
89 ctc cgc ttc aaa atc ctt cgc agc ctc cag gcc ttt gtg gct gta gcc 528
90 Leu Arg Phe Lys Ile Leu Arg Ser Leu Gln Ala Phe Val Ala Val Ala
91 140          145          150          155
93 gcc cgg gtc ttt gcc cat gga gca gca acc ctg agt ccc taa 570
94 Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Ser Pro
95          160          165
98 <210> SEQ ID NO: 2
99 <211> LENGTH: 189
100 <212> TYPE: PRT
101 <213> ORGANISM: Unknown Organism
103 <220> FEATURE:
104 <223> OTHER INFORMATION: surmised Homo sapiens
106 <400> SEQUENCE: 2
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108 -20          -15          -10
110 Ala Gln Gly Arg Ala Val Pro Gly Gly Ser Ser Pro Ala Trp Thr Gln
111 -5          -1 1          5          10
113 Cys Gln Gln Leu Ser Gln Lys Leu Cys Thr Leu Ala Trp Ser Ala His
114          15          20          25
116 Pro Leu Val Gly His Met Asp Leu Arg Glu Glu Gly Asp Glu Glu Thr
117          30          35          40
119 Thr Asn Asp Val Pro His Ile Gln Cys Gly Asp Gly Cys Asp Pro Gln
120          45          50          55
122 Gly Leu Arg Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile His Gln Gly
123 60          65          70          75
125 Leu Ile Phe Tyr Glu Lys Leu Leu Gly Ser Asp Ile Phe Thr Gly Glu
126          80          85          90
128 Pro Ser Leu Leu Pro Asp Ser Pro Val Ala Gln Leu His Ala Ser Leu
129          95          100          105
131 Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Gly His His Trp Glu Thr

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132          110          115          120
134 Gln Gln Ile Pro Ser Leu Ser Pro Ser Gln Pro Trp Gln Arg Leu Leu
135          125          130          135
137 Leu Arg Phe Lys Ile Leu Arg Ser Leu Gln Ala Phe Val Ala Val Ala
138 140          145          150          155
140 Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Ser Pro
141          160          165
144 <210> SEQ ID NO: 3
145 <211> LENGTH: 1203
146 <212> TYPE: DNA
147 <213> ORGANISM: Unknown Organism
149 <220> FEATURE:
150 <223> OTHER INFORMATION: Description of Unknown Organism: surmised Mus sp.
152 <220> FEATURE:
153 <221> NAME/KEY: CDS
154 <222> LOCATION: (113)..(700)
156 <220> FEATURE:
157 <221> NAME/KEY: mat_peptide
158 <222> LOCATION: (176)..(700)
160 <400> SEQUENCE: 3
161 cgcttagaag tcggactaca gagttagact cagaacccaaa ggaggtggat aggggggtcca 60
163 caggcctggg gcagatcaca gagccagcca gatctgagaa gcaggaaca ag atg ctg 118
164                                     Met Leu
165                                     -20
167 gat tgc aga gca gta ata atg cta tgg ctg ttg ccc tgg gtc act cag 166
168 Asp Cys Arg Ala Val Ile Met Leu Trp Leu Leu Pro Trp Val Thr Gln
169          -15          -10          -5
171 ggc ctg gct gtg cct agg agt agc agt cct gac tgg gct cag tgc cag 214
172 Gly Leu Ala Val Pro Arg Ser Ser Pro Asp Trp Ala Gln Cys Gln
173          -1 1          5          10
175 cag ctg tct cgg aat ctg tgc atg cta gcc tgg aac gca cat gca cca 262
176 Gln Leu Ser Arg Asn Leu Cys Met Leu Ala Trp Asn Ala His Ala Pro
177          15          20          25
179 gcg gga cat atg aat cta cta aga gaa gaa gag gat gaa gag act aaa 310
180 Ala Gly His Met Asn Leu Leu Arg Glu Glu Glu Asp Glu Glu Thr Lys
181 30          35          40          45
183 aat aat gtg ccc cgt atc cag tgt gaa gat ggt tgt gac cca caa gga 358
184 Asn Asn Val Pro Arg Ile Gln Cys Glu Asp Gly Cys Asp Pro Gln Gly
185          50          55          60
187 ctg aag gac aac agc cag ttc tgc ttg caa agg atc cgc caa ggt ctg 406
188 Leu Lys Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile Arg Gln Gly Leu
189          65          70          75
191 gct ttt tat aag cac ctg ctt gac tct gac atc ttc aaa ggg gag cct 454
192 Ala Phe Tyr Lys His Leu Leu Asp Ser Asp Ile Phe Lys Gly Glu Pro
193          80          85          90
195 gct cta ctg cct gat agc ccc atg gag caa ctt cac acc tcc cta cta 502
196 Ala Leu Leu Pro Asp Ser Pro Met Glu Gln Leu His Thr Ser Leu Leu
197          95          100          105
199 gga ctg agc caa ctg ctg cag cca gag gat cac ccc cgg gag acc caa 550

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200 Gly Leu Ser Gln Leu Leu Gln Pro Glu Asp His Pro Arg Glu Thr Gln
201 110          115          120          125
203 cag atg ccc agc ctg agt tct agt cag cag tgg cag cgc ccc ctt ctc 598
204 Gln Met Pro Ser Leu Ser Ser Ser Gln Gln Trp Gln Arg Pro Leu Leu
205          130          135          140
207 cgt tcc aag atc ctt cga agc ctc cag gcc ttt ttg gcc ata gct gcc 646
208 Arg Ser Lys Ile Leu Arg Ser Leu Gln Ala Phe Leu Ala Ile Ala Ala
209          145          150          155
211 cgg gtc ttt gcc cac gga gca gca act ctg act gag ccc tta gtg cca 694
212 Arg Val Phe Ala His Gly Ala Ala Thr Leu Thr Glu Pro Leu Val Pro
213          160          165          170
215 aca gct taaggatgcc caggttccca tggctaccat gataagacta atctatcagc 750
216 Thr Ala
217 175
219 ccagacatct accagttaat taaccatta ggacttggtc tgttcttggt tcgtttgttt 810
221 tgcgtgaagg gcaaggacac cattattaaa gagaaaagaa acaaacccca gagcaggcag 870
223 ctggctagag aaaggagctg gagaagaaga ataaagtctc gagcccttgg ccttggaagc 930
225 gggcaagcag ctgcgtggcc tgaggggaag ggggcggtgg catcgagaaa ctgtgagaaa 990
227 acccagagca tcagaaaaag tgagcccagg ctttggccat tatctgtaag aaaaacaaga 1050
229 aaaggggaac attatacttt cctgggtggc tcagggaaat gtgcagatgc acagtactcc 1110
231 agacagcagc tctgtacctg cctgctctgt ccctcagttc taacagaatc tagtcactaa 1170
233 gaactaacag gactaccaat acgaactgac aaa 1203
236 <210> SEQ ID NO: 4
237 <211> LENGTH: 196
238 <212> TYPE: PRT
239 <213> ORGANISM: Unknown Organism
241 <220> FEATURE:
242 <223> OTHER INFORMATION: surmised Mus sp.
244 <400> SEQUENCE: 4
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246 -20          -15          -10
248 Thr Gln Gly Leu Ala Val Pro Arg Ser Ser Ser Pro Asp Trp Ala Gln
249 -5          -1 1          5          10
251 Cys Gln Gln Leu Ser Arg Asn Leu Cys Met Leu Ala Trp Asn Ala His
252 15          20          25
254 Ala Pro Ala Gly His Met Asn Leu Leu Arg Glu Glu Glu Asp Glu Glu
255 30          35          40
257 Thr Lys Asn Asn Val Pro Arg Ile Gln Cys Glu Asp Gly Cys Asp Pro
258 45          50          55
260 Gln Gly Leu Lys Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile Arg Gln
261 60          65          70          75
263 Gly Leu Ala Phe Tyr Lys His Leu Leu Asp Ser Asp Ile Phe Lys Gly
264 80          85          90
266 Glu Pro Ala Leu Leu Pro Asp Ser Pro Met Glu Gln Leu His Thr Ser
267 95          100          105
269 Leu Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Asp His Pro Arg Glu
270 110          115          120
272 Thr Gln Gln Met Pro Ser Leu Ser Ser Ser Gln Gln Trp Gln Arg Pro
273 125          130          135

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275 Leu Leu Arg Ser Lys Ile Leu Arg Ser Leu Gln Ala Phe Leu Ala Ile
276 140          145          150          155
278 Ala Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Thr Glu Pro Leu
279          160          165          170
281 Val Pro Thr Ala
282          175
285 <210> SEQ ID NO: 5
286 <211> LENGTH: 102
287 <212> TYPE: PRT
288 <213> ORGANISM: Unknown Organism
290 <220> FEATURE:
291 <223> OTHER INFORMATION: Description of Unknown Organism: surmised Sus sp.
293 <400> SEQUENCE: 5
294 Ser Cys Leu Gln Arg Ile His Gln Gly Leu Val Phe Tyr Glu Lys Leu
295 1          5          10          15
297 Leu Gly Ser Asp Ile Phe Thr Gly Glu Pro Ser Leu His Pro Asp Gly
298          20          25          30
300 Ser Val Gly Gln Leu His Ala Ser Leu Leu Gly Leu Arg Gln Leu Leu
301          35          40          45
303 Gln Pro Glu Gly His His Trp Glu Thr Glu Gln Thr Pro Ser Pro Ser
304          50          55          60
306 Pro Ser Gln Pro Trp Gln Arg Leu Leu Leu Arg Leu Lys Ile Leu Arg
307 65          70          75          80
309 Ser Leu Gln Ala Phe Val Ala Val Ala Ala Arg Val Phe Ala His Gly
310          85          90          95
312 Ala Ala Thr Leu Ser Gln
313          100
316 <210> SEQ ID NO: 6
317 <211> LENGTH: 306
318 <212> TYPE: PRT
319 <213> ORGANISM: Homo sapiens
321 <400> SEQUENCE: 6
322 Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr
323 1          5          10          15
324 Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu
325          20          25          30
326 Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu Gly
327          35          40          45
328 Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
329          50          55          60
330 Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu
331 65          70          75          80
332 Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
333          85          90          95
334 Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys
335          100          105          110
336 Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr
337          115          120          125
338 Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln

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**VERIFICATION SUMMARY**

DATE: 02/13/2006

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TIME: 13:51:07

Input Set : A:\16622-005001.txt

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